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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/749,637A

DATE: 08/23/2001
TIME: 12:16:51

Input Set : A:\227a-rsq.txt
Output Set: N:\CRF3\08162001\I749637A.raw

3 <110> APPLICANT: University of Utah Research Foundation
 4 Cognetix, Inc.
 5 Olivera, Baldomero M.
 6 Cartier, G. Edward
 7 Watkins, Maren
 8 Hillyard, David R.
 9 McIntosh, J. Michael
 10 Layer, Richard T.
 11 Jones, Robert M.
 13 <120> TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
 15 <130> FILE REFERENCE: 2314-227
 17 <140> CURRENT APPLICATION NUMBER: US 09/749,637A
 18 <141> CURRENT FILING DATE: 2000-12-28
 20 <150> PRIOR APPLICATION NUMBER: US 60/243,412
 21 <151> PRIOR FILING DATE: 2000-10-27
 23 <150> PRIOR APPLICATION NUMBER: US60/219,440
 24 <151> PRIOR FILING DATE: 2000-07-20
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,263
 27 <151> PRIOR FILING DATE: 2000-06-26
 29 <150> PRIOR APPLICATION NUMBER: US 60/173,754
 30 <151> PRIOR FILING DATE: 1999-12-30
 32 <160> NUMBER OF SEQ ID NOS: 409
 34 <170> SOFTWARE: PatentIn version 3.0
 36 <210> SEQ ID NO: 1
 37 <211> LENGTH: 261
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Conus gloriamaris
 41 <220> FEATURE:
 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (1)..(231)
 45 <400> SEQUENCE: 1
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 47 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 48 1 5 10 15
 50 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt 96
 51 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
 52 20 25 30
 54 ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat ccg 144
 55 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
 56 35 40 45
 58 gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192
 59 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
 60 50 55 60
 62 aac tgc tgc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaaactacc
 63 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
 64 65 70 75
 66 gtgatgtctt ctctccccctc 261

ENTERED

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Input Set : A:\227a-rsq.txt

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68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 77
 70 <212> TYPE: PRT
 71 <213> ORGANISM: Conus gloriamaris
 73 <400> SEQUENCE: 2
 74 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 75 1 5 10 15
 77 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
 78 20 25 30
 80 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
 81 35 40 45
 83 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
 84 50 55 60
 86 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
 87 65 70 75

89 <210> SEQ ID NO: 3
 90 <211> LENGTH: 29
 91 <212> TYPE: PRT
 92 <213> ORGANISM: Conus gloriamaris
 94 <220> FEATURE:
 95 <221> NAME/KEY: SITE
 96 <222> LOCATION: (1)..(29)
 97 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp or bromo-Trp

101 <400> SEQUENCE: 3
 W--> 102 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
 103 1 5 10 15
 W--> 105 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
 106 20 25

108 <210> SEQ ID NO: 4
 109 <211> LENGTH: 29
 110 <212> TYPE: PRT
 111 <213> ORGANISM: Conus gloriamaris
 113 <220> FEATURE:
 114 <221> NAME/KEY: SITE
 115 <222> LOCATION: (1)..(29)
 116 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 22 may be Trp or bromo-Trp

121 <400> SEQUENCE: 4
 W--> 122 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln
 123 1 5 10 15
 W--> 125 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
 126 20 25

128 <210> SEQ ID NO: 5
 129 <211> LENGTH: 29
 130 <212> TYPE: PRT

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Input Set : A:\227a-rsq.txt
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131 <213> ORGANISM: Conus gloriamaris
 133 <220> FEATURE:
 134 <221> NAME/KEY: SITE
 135 <222> LOCATION: (1)..(29)
 136 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at
 residue
 137 e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
 138 or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, L-
 139 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 141 <400> SEQUENCE: 5
W--> 142 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
 143 1 5 10 15
W--> 145 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
 146 20 25
 148 <210> SEQ ID NO: 6
 149 <211> LENGTH: 542
 150 <212> TYPE: DNA
 151 <213> ORGANISM: Conus omaria
 153 <220> FEATURE:
 154 <221> NAME/KEY: CDS
 155 <222> LOCATION: (146)..(235)
 157 <400> SEQUENCE: 6
 158 gaagctggta cgcctgcagg taccggtccg gaattcccg gtcgacatca tcatacatcga 60
 160 tccatctgtc catccatcca ttcatcatt cgctgccaga ctataataaa cattcaagtc 120
 162 tctttttttt ttttgtctg acaga tcg atc agg atg tgc cgt aga gaa gct 172
 163 Ser Ile Arg Met Cys Arg Arg Glu Ala
 164 1 5
 166 caa ctt tgt gat ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc 220
 167 Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
 168 10 15 20 25
 170 gtt ttg gtc tgc gtc taaaactacc gtgtatgtctt ctcctccct ctagtagtag 275
 171 Val Leu Val Cys Val
 172 30
 174 taggcggccg ctctagagga tccaaacctt cgtacgcgtg catgcgacgt catagcttt 335
 176 ctatagtgtc acctaaattc aattcaactgg cgcgtttt acaacgtcgt gactggaaaa 395
 178 accctggcgt tacccaaactt aatcgccctt cagcacatcc cccttcgccc agctggcgt 455
 180 atagcgaaga ggccccgacc gatgcgcctt cccaaacagt ggcgcgcgtt aatggcgaat 515
 182 gggacgcgcc ctgttagcggc gcattat 542
 184 <210> SEQ ID NO: 7
 185 <211> LENGTH: 30
 186 <212> TYPE: PRT
 187 <213> ORGANISM: Conus omaria
 189 <400> SEQUENCE: 7
 190 Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
 191 1 5 10 15
 193 Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val
 194 20 25 30
 196 <210> SEQ ID NO: 8
 197 <211> LENGTH: 27
 198 <212> TYPE: PRT

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199 <213> ORGANISM: Conus omaria
 201 <220> FEATURE:
 202 <221> NAME/KEY: SITE
 203 <222> LOCATION: (1)..(27)
 204 <223> OTHER INFORMATION: Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue
 11 m

205 ay be Pro or hydroxy-Pro

207 <400> SEQUENCE: 8

W--> 208 Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys

209 1 5 10 15

211 Cys His Gly Leu Phe Cys Val Leu Val Cys Val

212 20 25

214 <210> SEQ ID NO: 9

215 <211> LENGTH: 346

216 <212> TYPE: DNA

217 <213> ORGANISM: Conus textile

219 <220> FEATURE:

220 <221> NAME/KEY: CDS

221 <222> LOCATION: (25)..(315)

223 <400> SEQUENCE: 9

224 ggcatatcac aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt 51

225 Met Lys Leu Thr Cys Met Met Ile Val

226 1 5

228 gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc 99

229 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser

230 10 15 20 25

232 aqa aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147

233 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu

234 30 35 40

236 aac ctc gaa gac tct aaa cac agg cac cag qag aga ccg gac acc ggc 195

237 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly

238 45 50 55

240 gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243

241 Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys

242 60 65 70

244 gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291

245 Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp

246 75 80 85

248 tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactccat 345

249 Tyr Cys Val Val Leu Ser Cys Thr

250 90 95 346

252 c

254 <210> SEQ ID NO: 10

255 <211> LENGTH: 97

256 <212> TYPE: PRT

257 <213> ORGANISM: Conus textile

259 <400> SEQUENCE: 10

260 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

261 1 5 10 15

263 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Met Glu Asn Leu

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Input Set : A:\227a-rsq.txt

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264 20 25 30
 266 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His
 267 35 40 45
 269 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
 270 50 55 60
 272 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
 273 65 70 75 80
 275 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys
 276 85 90 95
 278 Thr
 280 <210> SEQ ID NO: 11
 281 <211> LENGTH: 31
 282 <212> TYPE: PRT
 283 <213> ORGANISM: Conus textile
 285 <220> FEATURE:
 286 <221> NAME/KEY: SITE
 287 <222> LOCATION: (1)..(31) *t*
 288 <223> OTHER INFORMATION: Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4
 may be
 289 Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-
 290 Glu; Xaa at residue 23 may be Trp or bromo-Trp; Xaa at residue 24
 292 <220> FEATURE:
 293 <221> NAME/KEY: SITE
 294 <222> LOCATION: (1)..(31) *t*
 295 <223> OTHER INFORMATION: may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-
 Tyr
 296 or O-phospho-Tyr
 298 <400> SEQUENCE: 11
W--> 299 Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Ile Phe
 300 1 5 10 15
W--> 302 Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr
 303 20 25 30
 305 <210> SEQ ID NO: 12
 306 <211> LENGTH: 265
 307 <212> TYPE: DNA
 308 <213> ORGANISM: Conus omaria
 310 <220> FEATURE:
 311 <221> NAME/KEY: CDS
 312 <222> LOCATION: (1)..(234)
 314 <400> SEQUENCE: 12
 315 atg aaa ctg acg tgc ctg atg atc gtt gcc gtg ctg tcc ttg acc ggc 48
 316 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
 317 1 5 10 15
 319 tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt 96
 320 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
 321 20 25 30
 323 ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
 324 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
 325 35 40 45
 327 aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa 192
 328 Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\227a-rsq.txt
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L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
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L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:1648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

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L:1718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69